

GapServer version 5.1.1
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OM nucleic - nucleic search, using sw model

Run on: January 14, 2003, 11:42:22 - Search time of All: seconds
(without alignments)
11136.303 Million cell updates/sec

Title: us-09-910-428-1

Perfect score: 26

Sequence: 1 gtagctaatccttctctgtacacag 26

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues 32308152

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: EST:
1: em_estla.*
2: em_estlum.*
3: em_estlin.*
4: em_estlm.*
5: em_estec.*
6: em_estpl.*
7: em_estro.*
8: em_estl.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_luv.*
20: em_gss_pla.*
21: em_gss_vit.*
22: em_gss_fun.*
23: em_gss_mam.*
24: em_gss_mus.*
25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_rtd.*

Prod % is the number of results predicted by Sharon's have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	19.8	76.2	458 14	BQ3977777 NISC_Anc2
2	19.8	76.2	492 12	Bf513573 Hf513573
3	19.8	76.2	549 10	AM644499 CM41H03.W
4	19.8	76.2	566 12	Bf071855 db47d03.x
5	19.8	76.2	707 14	BQ188518 HT-F-ETI-
6	19.8	76.2	718 13	Bf089332 Bf089332

Result	Score	Query Match Length	DB ID	Description
7	19.6	75.4	862 9	AAT98980
8	19.6	75.4	305 17	CNS0281
9	19.6	75.4	540 10	AV898440
10	19.2	73.8	803 13	B1461824
11	19.2	73.8	1083 17	CNS0388P
12	19.2	73.8	370 17	A2731725
13	18.8	72.3	372 13	B1321744
14	18.8	72.3	516 13	B1964629
15	18.8	72.3	626 13	B1964625
16	18.8	72.3	701 10	AM104045
17	18.8	72.3	796 17	HM718132
18	18.6	71.5	234 10	AM417202
19	18.6	71.5	271 9	AV131634
20	18.6	71.5	388 17	B63995
21	18.6	71.5	471 13	B1898647
22	18.6	71.5	476 13	BM483804
23	18.6	71.5	508 10	AV663308
24	18.6	71.5	514 13	BM088926
25	18.6	71.5	517 13	BM253554
26	18.6	71.5	530 12	BE809805
27	18.6	71.5	542 12	HM751000
28	18.6	71.5	539 12	HM752343
29	18.6	71.5	548 10	AM660350
30	18.6	71.5	558 10	AV791824
31	18.6	71.5	550 12	BE750323
32	18.6	71.5	564 13	B1535110
33	18.6	71.5	574 13	B1773779
34	18.6	71.5	602 13	B1535654
35	18.6	71.5	651 10	BM649754
36	18.6	71.5	768 17	AG097938
37	18.6	71.5	843 17	CNS07961
38	18.6	71.5	941 17	A2136491
39	18.2	70.0	390 12	A2598292
40	18.2	70.0	548 17	A2976761
41	18.2	70.0	564 17	A2382534
42	18.2	70.0	567 12	BE940874
43	18.2	70.0	593 9	A1857121
44	18.2	70.0	632 17	BM761980
45	18.2	70.0	655 17	BH051439

ALIGNMENTS

RESULT 1
BQ3977777
LOCUS
DEFINITION
NISC_mnc2302 y1 Soares NMEG Xenopus laevis cDNA clone IMAGE:5161995
5', mRNA sequence.
BQ3977777
BQ3977777.1 GI:21085464
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Xenopus laevis
African clawed frog.
REFERENCE
1 (bases 1 to 458)
NISC_mnc2302 y1 Soares NMEG Xenopus laevis cDNA clone IMAGE:5161995
TITLE
African clawed frog
JOURNAL
COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cyprus-remail.nih.gov
cDNA Library Preparation: M. Hertz Soares (University of Iowa)
cDNA Library Arrayed by: The J.M.A.G.E. Consortium/LLNL at:
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone Distribution: NCI CGAP clone distribution information can be
found through the J.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: LLML1402 row: A column: 4
Seq primer: M13RF1 reverse primer (Abi).

Lettera di committente

Query Match:	76.2%	Score 19.46	EMB 14	Length 458,
Best Local Similarity:	91.3%	Pred. No. 4.1e+02		
Matches	21	Conservative	2	Indels 0; Gaps 0;
		Mismatches	2	

LOCUS	HP514573	492 bp	mRNA	linear	EST 07-DEC-2000
-------	----------	--------	------	--------	-----------------

1

[illegible][illegible]

ay	2	TCGTCGATCTTTTCGCTACCA	24
Dh	272	TCGCTATCTTTTCGCTCTTA	294

100

(IMAGE clones) 132911-132504), 1471348-1472903,
1492104-1493255). NCI-GCAP-Lens pool 1 LHM 1576-3592,
3851-3854 (IMAGE clone IDs 141925-141791, 152904-1525439),
); NCI-GCAP-GS4 pool 1 LHM 4164-4167, 4716-4720,
3733-3735 (IMAGE clone IDs 1257976-1258631, 1469064-147098
1475592-14757743); NCI-GCAP-FR22 pool 1 LHM 2457-2459,
2758-2759, 3022-3058 (IMAC clone IDs 985608-986759,
1101192-1101959, 1217928-1220615); NCI-GCAP-F20 pool 1
LHM 2644-2653, 2871-2872 (IMAGE clone IDs 2077416-2081255,
1144584-1145351). (6% of the driver population), plus a
pool of 3,840 arrayed clones from NCI-GAP-Side (IMAGE
clones 279816-279835) and NCI-GAP-Side2 (IMAC
clone ID 2710536-2712455) (4% of the driver population
); plus a pool of 11,136 clones from NCI-GCAP-Side (IMAC
clones 2713456-2723592) (13% of the driver population),
plus a pool of 5,472 clones from NCI-GCAP-Side4 (IMAGE
clone IDs 2723592-2729326) (40% of the driver population),
plus a pool of 4032 clones from NCI-GCAP-Side (IMAC
clones 2728969-2733190) (40% of the driver population).
Subtraction was performed as previously described (Bonaldi
& Lennon & Soares (1996): Normalization and Subtraction:
Two Approaches To Facilitate Gene Discovery, Genome
Research 6, 791-806.
TAG_Seq=None found".

	124 a	125 c	119 g	123 t	1 others
ch	76.2%	Score 19.8;	DB 12;	Length 492;	
1 Similarity	91.3%	Pred. No.	4.2e+02;		
21:	Conservative	0;	Mismatches	2;	Indels 0;
GCTCAATGTTTTCGTACGA 24					
CCTCATATTCTTCTCGTCTTA 294					

AM644499 549 bp mRNA linear EST 26-APR-2001
cm4l03.wt BlackShear/Stages normalized Xenopus egg library Xenopus
laevis CDNA clone PBX0140H03 5', mRNA sequence.
AM644499
AM644499.1 GI:7401888
EST:
Allian clawed frog.
Xenopus laevis
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Amphibia: Batrachia: Anura: Mesobatrachia: Pipridae: Pipidae;
Xenopodinae: Xenopus.
1 (bases 1 to 549)
BlackShear,F.D., Lauder,M.S., Thoenig,M., Reinhardt,E.A., Stalla,N.,
Jr., Moore,D.T., Boulard,G.B., Beckstrom-Sternberg,S.M., Touchman
J.W., Bonaldi,M.F. and Soares,M.B.:
The NIH XENOPUS Multitask EST Project: cloning analysis of the
first 13,879 ESTs from unfertilized eggs
Gene 267 (1): 71-87 (2001)
2111403
Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory at National Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
USA
Tel: 919 541-4899
Fax: 919 541-4571
Email: blackp00@niehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
Phone 800 533-3361 ext.cdn, fax 256-536-9016 att:cna, email
cdnaresgen.com
DNA sequencing and analyses performed by National Institutes of
Health Intramural Sequencing Center (NISC).
PCR Primers
FORWARD: TGTAAAGCAGCCGCAC

BACKWARD: CAGGAAACGCTATGACC
 Plate: 0140 Row: H Column: 03
 Seq primer: 17 primer.
 Location/Qualifiers
 1. 549

/organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="PBX0140H03"
 /issue="11b" Blackshear/Sources normalized Xenopus egg
 library
 /sex="female"
 /issue_type="unfertilized egg"
 /cell_type="unfertilized egg"
 /dev_stage="unfertilized egg"
 /lab_host="DH10B"

/note="Vector: pT73 Pac, Site_1: EcoRI, Site_2: NotI; PolyA-selected mRNA was prepared from unfertilized Xenopus laevis eggs. The library was constructed in the vector pT73-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. 'Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-d18 primer; double stranded cDNAs were ligated to EcoRI adapters, digested with NotI, and directionally cloned into the NotI and EcoRI-digested pT73 Pac vector. The library contained approximately 7.2 X 10⁵ recombinants, with average insert sizes of 1-1.5 kb."
 BASE COUNT 179 a 86 c 112 g 172 t
 ORIGIN

Query Match 76.2% Score 19.8; DB 10; Length 549;
 Best Local Similarity 31.3% Fred. No. 4.3e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

cy 1 CTCCTCAATCTTTCCTGACC 23
 ||||||||| ||||| |||||
 Db 242 GTCTCAATCTTTCCTGACC 264

RESULT 4
 BP071855/c 566 bp mRNA linear EST 17-OCT-2000
 LOCUS 047403 x1 R1a-kshpar/Sources normalized Xenopus egg library Xeno-fus
 DEFINITION laevis cDNA clone IMAGE:3301637 3', mRNA sequence.
 ACCESSION BP071855
 KEYWORDS BP071855.1 GI:10848494
 EST
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Anura; Anura; Mesobatrachia; Pipridae; Pipridae;
 Xenopodidae; Xenopus.
 1 (bases 1 to 566)
 AUTHORS Clifton S. Johnson, S. L. Rumberg R. Song, T. Hillier, L. Pape, D.
 Martin, J. J. Wyllie, T. Underwood, K. Theisling, B. Bowers, Y. Peterson
 B. Gildous, M. Harvey, N. Riller, E. Jackson, Y. McCann, R.
 Waterston, R. and Wilson, R.
 TITLE Washu Xenopus EST project, 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: Sandy Clifton, Ph.D.
 Washu Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 9501 St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 Library constructed by Bento Soares and M. Fatima Bonaldo
 (University of Iowa). DNA sequencing by: Washington University
 Genome Sequencing Center
 Genome Sequencing Center
 through the I.M.A.G.E. Consortium/Jan. at: int@imgc.llnl.gov
 Seq primer: -400P from Gibco
 High quality sequence stop: 458.

FEATURES
 source

Location/Qualifiers
 1. 566
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="IMAGE:3301637"
 /issue="11b" Blackshear/Sources normalized Xenopus egg
 library
 /sex="female"
 /issue_type="unfertilized egg"
 /cell_type="unfertilized egg"
 /dev_stage="unfertilized egg"
 /lab_host="DH10B"

/note="Vector: pT73-Pac, Site_1: EcoRI, Site_2: NotI; PolyA-selected mRNA was prepared from unfertilized Xenopus laevis eggs. The library was constructed in the vector pT73-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. 'Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-d18 primer; double stranded cDNAs were ligated to EcoRI adapters, digested with NotI, and directionally cloned into the NotI and EcoRI-digested pT73-Pac vector. The library contained approximately 7.2 X 10⁵ recombinants, with average insert sizes of 1-1.5 kb."
 BASE COUNT 180 a 114 c 85 g 187 t
 ORIGIN

Query Match 76.2% Score 19.8; DB 12; Length 566;
 Best Local Similarity 91.3% Fred. No. 4.3e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

cy 1 GTCTCAATCTTTCCTGACC 23
 ||||||||| ||||| |||||
 Db 314 GTCTCAATCTTTCCTGACC 292

RESULT 5
 B0188518/c 707 bp mRNA linear EST 30-APR-2002
 LOCUS B0188518
 DEFINITION UI-E-EJ1-ajw-h-18-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone
 ACCESSION B0188518
 KEYWORDS B0188518 GI:20364059
 EST
 SOURCE human.
 ORGANISM Homo sapiens
 REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 707)
 AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Rockstrom Medical Research Building Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: msoares@blue.weeg.uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 REVERSE.

FEATURES
 source

Location/Qualifiers
 1. 707
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="UI-E-EJ1-ajw-h-18-0-UI"

ZELSER LIB-01 E.E.I.*

Oligo eye: total eyes; Optic nerve; retina; Retina Foveal and Macular; RPE and Choroid.

Abs strage = "total and adult"

Gab host plasmid (Life Technologies) (in phage vector)*

Gene target eye: Vector from PstI (PfuII restriction site) modified polylinker Site 1; EcoR I; Site 2; Not I;

(U.E.B.) Is a subtracted cDNA library constructed according to Honaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pTT7-Pac vector. The oligonucleotide used to prime the synthesis of first strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)₁₈ tail. The respective large scale libraries are: total eyes, ACANTACAT; lens, CATANACTA; eye anterior segment, AATCCCATC; optic nerve, CCACTAACG; retina, GCGGG; Retina Foveal and Macula, GTTC; RPE and choroid, ACCGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).*

167 d 188 g 178 t 2 others

BASE COUNT	(Mollusca/CRG Institute), *				clasts
ORIGIN	241.4	241.3	240.4	22.1	
Clarity Match					
Best Local Similarity	76.28	Score 19.8	DB 13	length 718	
Mat. loc.	22	Conservative	6	Manual loc.	2
				Trunks	0
				caps	0
Q7	1	GCGCTAATCTTTCTCTCAAC	23		
		TTTTTTTTTTTTTTTTTTTT			
DB	285	GTCCTAATCTTTCTCTCAAC	253		

BASE CONTENT	24.6	24.7	28.9	22.1					
ORIGIN	(Mellon/CRC Institute), "								
Query Match	76.2%	Score 19.81	DH 131	Length 718;					
Esp Local Similarity	91.3%	Prod No. 473002							
Mat Loc	22	Conservation	C	Mismatch	22	Indels	0	Gaps	0
CY	1	CTCCTCAATCTTTCCTCAAC	23	TTTTTTTTTT	TTTTTTTT				
DB	285	GTCTCAATCTTTCCTCAAC	263						
RESULT 7									
AAT98980/c		862 bp	mRNA	Unnot	EST ID-FR-1398				
Locus	V95F02.71	Stratagene mouse skin (#97113)			Mus musculus cDNA clone				
DEFINITION	IMAGE:338271.5'	similar to db:339040 SPARC_FRODOKSTR (CHUMAN);							
	db:X04017	Mouse mRNA for cysteine-rich glycoprotein SPARC (MOUSE);							
		AA798980							
VERSION	AAT98980								
KEYWORDS	AAT98980.1	GI:2861935							
SOURCE	FST.								
ORGANISM	house mouse,								
	Mus musculus								

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eikaraya, I. Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus 1 (Bases 1 to 86)

Morris, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubouque, T., Giesel, S., Kuehba, T., Lacy, M., Le, M., Martin, J., Morris, M., St-Helbert, R., Stedler, M., Tan, F., Woodward, K., Moore, B., Theising, B., Wyle, T., Lennon, G., Soares, E., Wilson, R. and Worston, R.

The MASHU HMM Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project

Washington Mouse Est Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel.: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through INT: contact the
IMMSE Consortium (info@immse.intl.gov) for further information.
MGI:655763
Seq primer: -28nt3 rev1.17 from Amersham
High quality sequence stop 408.

```

FEATURES
SOURCE
LOCATION/Qualifiers
1. H62
/organism-"Mus musculus"
/strain-"C57BL/6"
/pub_med-"(taxon:10090)"
/feature-"IMAG:1210171"
/feature_list-"stratagene mouse skin (#97713)"
/sex-"females"
/misc_type-"whole skin"
/dev_stage-"11 weeks old"
/lab_host-"SQU (kanamycin resistant)"
/photo-"clean skin, white, ethanolic 95% alcohol"

```

	Site 2: Klot; cloned unidirectionally	Primer: colligo
	d. whole skin from 11 week old female mice.	
	Average insert size: 1.0 kb; Uni-ZAP XR Vector:	5'
	adapter sequence: 5' GAATTCGACAG 3'	3' adapter
	sequence: 5' CTCGACTTCTTTTCTTTT 4''	
BASH COUNT	194 c	244 g 175 t
ORIGIN		

Query Match	75.4%	Score 19.6	EB 7	Length 822
Host: Local Similarity	84.6%	Pred. No. 60.92		
Matches	22	Conservative	0	Mismatches 4
			Indels	0
			Gaps	0
QY	1	GTGGCTAACTCTTCTGTAACAG	26	

Db 626 GCGCCGCAACGCTCTGCTGACCAAG 601

RESULT 8
CNS022R1 905 bp DNA linear GSS 15-MAY-2000
LOCUS Tetradodon nigroviridis genome survey sequence TNC001 end of clone
DEFINITION 183001 of library G from Tetradodon nigroviridis, genomic survey
sequence

ACCESSION
VERSION AL221319.1 GI:7880138
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradodon nigroviridis.
ORGANISM Tetradodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Perciformes; Tetraodoniformes;
Tetraodontidae; Tetraodon.

REFERENCE
AUTHORS Roest-Collins H., Jallou O., Dasilva C., Fizes C., Fisher C.,
Bernot A., Fizes C., Wincker P., Brolier F., Quetier F.,
Saurin W. and Weissenbach J.
Human gene number estimate provided by genome wide analysis using
Tetradodon nigroviridis DNA sequence

TITLE Unpublished

JOURNAL, REFERENCE 2 (bases 1 to 905)
AUTHORS Roest-Collins H., Jallou O., Dasilva C., Fizes C., Fisher C.,
Bernot A., Fizes C., Wincker P., Brolier F., Quetier F.,
Saurin W. and Weissenbach J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradodon nigroviridis

GENOSCOPE
3 (bases 1 to 905)

Direct Submission
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large
scale clone and sequencing project of the Tetradodon nigroviridis
genome. For more information, please take a look at
<http://www.genoscope.cns.fr/Tetraodon>

FEATURES
SOURCE
LOCATION/Qualifiers
1..905
/organism="Tetradodon nigroviridis"
/db_xref="taxon:99883"
/clone="183001"
/clone_1lb="G"
/note="Genoscope sequence ID: CNS022R1SP1-end"
pur="ori"

BASE COUNT 212 c 208 g 226 y 262 t 2 others

ORIGIN

Query Match 75.4%, Score 19.6; DB 17; Length 905;
Best Local Similarity 84.6%; Pred. No. 6, le-02;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Caps 0;

Db 252 CTGCTTAACTCTGCTGACCAAG 277

RESULT 9
AVB89040 580 bp mRNA linear EST 09-NOV-2001
LOCUS AVB89040 Nori Satoh unpublished cDNA library, cleavage stage embryo
DEFINITION AVB89040 Nori Satoh unpublished cDNA clone rcic31104 3', mRNA sequence.
ACCESSION
VERSION AVB89040
KEYWORDS EST.
SOURCE Clona intestinalis.
ORGANISM Clona intestinalis
Eukaryota; Metazoa; Chordata; Prochordata; Ascidiacea; Enteropneua;
Phlebobranchia; Clonidae; Clona

REFERENCE 1 (bases 1 to 580)

AUTHORS Satoh, N., Satou, Y., Kohara, Y., and Shin, I.
Expressed genes in Clona intestinalis
Unpublished (2000)
JOURNAL Contact: Nori Satoh
COMMENT Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
E-mail: satoh@zoo.kyoto-u.ac.jp

FEATURES
SOURCE
LOCATION/Qualifiers
1..580
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="rcic31104"
/clone_1lb="Nori Satoh unpublished cDNA library, cleavage
stage embryo"
/tissue_type="whole animal"
/dev_stage="cleavage stage embryo"
/note="Vector: pBluescript SK"

BASE COUNT 159 a 98 c 94 g 188 t 1 others

ORIGIN

Query Match 75.8%; Score 19.2; DB 10; Length 580;
Best Local Similarity 87.5%; Pred. No. 7, 9e-02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Caps 0;

Db 290 GCGCGCAACGCTCTGCTGACCA 313

RESULT 10
B1461824 803 bp mRNA linear EST 21-AUG-2001
LOCUS B1461824
DEFINITION U03207531F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5274287 5',
mRNA sequence.
ACCESSION B1461824
VERSION B1461824.1 GI:15252480
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 803)
NIH-MGC B1P://mgs-nci.nih.gov/
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: Miklos Palcovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NIH/RI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMNI)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
<http://image.llnl.gov>
Plate: LLAM1689 row: n column: 08
High quality sequence stop: 761.
LOCATION/Qualifiers
1..803
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5273387"
/clone_1lb="NIH_MGC_97"
/lab_host="DH10R"
/note="Organ. testis, Vector: pBluescript (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI; XhoI (quecag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN 3',
size-selected for average insert size 2.2 kb and
normalized to 10^5. This is a primary library enriched
for full-length clones and constructed using the

Accepted for publication 15 September 2002
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 J. Mass Spectrom. 38, 1339–1342 (2003)
 DOI: 10.1002/jms.1000

BASE CATALYST	202 A	155 C	133 G	312 I	1 C; here
ORIGIN					

	Diversity	74.8%	Score 19.22	DB 132	Length 803
	Host Local Similarity	H7.5M	Pred. No. 8.7e+02		
	Matches	22	(percentage)	3	Total 2, Gap 5
Cy	I GGGTGAATCTTTCTGAGAA	24			
	TTTTTTTTTTTTTTTTTTTT				
Dib	TGCGACTAATCTTCCTCAATAA	39			

	RESULT 11
CMS ABCE/c ^a	
L/ratio	
DEFINITION	
n=869 0000	108 k bp DNA 25S 15-MAY-2000
Tetradation microsatellites genome survey sequence 7' end of clone .	

with 10 of 1 library c from *Tetradodon nigrovittatus*, genomic survey sequence.

ACCESSION	ALZ36302
VERSION	ALZ36302.1 GI:7895437
KEYWORDS	GSS; genome survey sequence.

SOURCE: Tetradon nigroviridis (ORGANISM)

REFERENCES
1 (bases 1 to 1083)

AUTHORS	TITLE
ROBERTS TROLLIUS, H., JALLON, O., DASTI, C., BOMMEAU, L., FISHER, C., HERRIOT, A., FIZANEZ, C., MUCKER, P., BROUILLER, P., QUELLIER, F., SAUTIN, W. and WEISSENBACK, J.	Human gene number estimated by genomic wide analysis using tetraodon microvittids DNA sequence

REFERENCE

Rosenblatt, H., & Miller, G. (1980). *Planned vs. Elected C.*. Unpublished working paper (bases 1 to 1083).

TITLE Characterization and repeat analysis of the freshwater pufferfish tetraodon nigrofasciatus
 JOURNAL J. Heredity
 REFERENCE 3 (bases 1 to 1983)

ADDITIONAL INFORMATION:
 TITLE: *Genoscope: Submision Direct Submission*
 JOURNAL: *Submitted (12 APR-2000)*
 COMMENT: This sequence is a single read and was generated as part of a large scale clone- and sequencing project of the tetraodon nigrovittatus genome. For more information, please take a look at <http://www.genoscope.cnr.fr/tdo/>

FEATURES	LOCATION/QUALITIES
SOLUBLE	1. -1084
	forantism."foradodan nigroviridiths"
	zab xrtat "taxos 99883"
	/elone "011E10"
	/elone lib-"67"
	/elone "Gomogrope" sequence ID: G086011W05LE1 end: 77"
BASE COUNT	455 a 234 c 172 g 274 t 29 others
ORIGIN	

Only Match	73.8%	Score 19.2	DB 17	Length 1083
First Local Similarity	80.8%	Prod. No. 9.5e+02		
Matched	212	Construct 1	Minim 4	Index 2
UY	1	GTGGTAACTTCTCTGATCACT	26	
	11	1111111111111111		
DB	427	GTTCTTAACTTTTCTGATCACT	302	

RESUB 12
A7731725

LOCUS	A731725	370 bp	10000	328 25 JAN 2001
DEFINITION	Mus musculus genomic clone: 24 M18 mus24.1			
ACCESSION	A731725			
VERSION	A731725.1	GI:12494053		

ACCESSION	A2731725
VERSION	A2731725.1 GI:12494054

KEYWORDS	GSS.
SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE
1 (bases 1 to 370)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

COMMENT	JOURNAL	TITLE	AUTHORS
Other_5555: RPCT-24-84D24, TVB		Mouse BAC End Sequences from Library RP1.24	Shafman, S., Tschape, S., Notman, W., Mallick, R., Tschape, S., Gock, K., Kroll, M., Shoulsberg, A., Russell, D., de Jong, P., and Fraser, C. M.
		Unpublished (1991)	

Contact: Jianfeng Zhao
Department of Biogeriatric Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 848 0200
Fax: 301 848 0208

Email: szhao@ligr.org
 Clones are derived from
 library availability,

(paleont@mail.cfo.org). Clothes may be purchased from RACPA's *Resources* (<http://www.cfo.org/clothes/order.html>). BAC's online page, http://www.cfo.org/followup/ends-on-ns-bac_end_intro.html

plate: 84 row: 1 column: 2
Seq primer: SP6
Class: HAC ends.

FEATURES	Location/Qualifiers
SOURCE	1. 370
	Location "MUSCULUS"
	/strain="C57H/6J"

```
/db_xref="taxon:10090"  
/clone="RRC1_24-84D24"  
/locus_tag="RRC1_24"
```

```

/sex="Male"
/cell_type="Spleen/Brain"
/notes="Vet 601: P1ANBAC1, Site 1: BAMB1;
RPI: 24 Mouse BAC library produced by Peter de Jong. The
library was cloned in the P1ANBAC1 cloning vector at the
BamHI sites using MspI partially digested male C57BL/6J

```

	DNA ^a
BASE CONTENT	139 a 49 c 69 g 113 t
ORIGIN	
Couffy Match	72-88;
BEST LOCAL SIMILARITY	Pred. No. 1e+03;
Mutates w/ Concomitant	2; Mutations = 2; Indels = 0; Gaps = 0

5' - GTGGTCTAATGCTTTCTGGTAC 22
 11111111 1111 111111
 3' - GTGGTCTAAGCTTTTCTGTAAC 302

RESULT 13
 b1321744
 81321744 372 bp mRNA 110661 EST 29-NOV-2005

DEFINITION	ss4796d12.y1 gm c13779 glycylic max cDNA clone genome sytems
ACCESSION	U01009
VERSION	1
KEYWORDS	EST
SOURCE	soybean
ORGANISM	Glycine max
	Elavay-33, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta

REFERENCE
1 (bases 1 to 372)

Host Local Similarity: 90.98; Prod. No. 1.1e+03;
Matches: 20; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0.

QY 5 TCTAATCTTTTCGTACACAG 26
IIIIIIIIIIIIIIIIIIII
DB 170 TCTAATCTTTTCGTACACAG 191

RESULT 15

B1969065

FEATURES

DEFINITION

VERSION

KEYWORDS

SOURCE

ORGANISM

glycine max

glycine max

glycine max

glycine max

glycine max

glycine max

glycine max

glycine max

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Gm-1083 library is listed in the 'OTHER EST' field. The
detailed information on the source library for each clone
can also be obtained by referring to the Inyte Genomes
clone ID of the original cDNA library that is also listed
under 'OTHER EST'.

Query Match: 72.4%; Score 18.8; DB 1.1; Length 6,26;
Host Local Similarity: 90.98; Prod. No. 1.1e+03;
Matches: 20; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0.

QY 5 TCTAATCTTTTCGTACACAG 26
IIIIIIIIIIIIIIIIIIII
DB 251 TCTAATCTTTTCGTACACAG 272

Search completed: January 14, 2003, 15:10:27
Job time: 41.8117 secs

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1. (bases 1 to 626)
Wadkin, L., Krimm, R., Shewmaker, R., Beckwith, E., Khanna, A., Goyell, V.,
Friedman, J., Rapp, C., Shoop, E., Pardinas, J., Lin, L., and Lowin, H.
A functional genomics program for soybean (NSP 9872565)
Unpublished (1999)
on her ESTs: AW203558 corresponding to Gm-c1028-1970 (5')
Contact: Wadkin, L.O., PI, A Functional Genomics Program for
Soybean (NSP 9872565)
Lowin, H. A., Director, Keck Center for Comparative and Functional
Genomics
University of Illinois
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147
Fax: (217) 333-4582
Email: l.wadkin@uiuc.edu
This clone is available through: Inyte Genomes, 4633 World
Parway Circle, St. Louis, Missouri 63144, Phone (800) 439-0030 or
(314) 427-3222 FAX: (314) 427-3324, Web site:
http://www.inyte.com/rapid/rapid4273324/rapid4273324.html
n/index
Seq primer: 5' TTTTCTTTTCTTTTCTTTT(A/C/C)-3'
Location/Qualifiers

L: 626

/organism="glycine max"

/db_xref="taxon:3847"

/clone="Gm-1083 2360"

/clone_lib="Gm-1083"

Note: The library Gm-1083 is a sequence-driven, retracted
set of 4,992 clones selected from cDNA libraries from
various tissues and stages of development of soybean. It
represents 117 sequences from the progenitor library
Gm-c1009 (from mature roots of 2 month old greenhouse
grown 'Williams' soybean plants); 820 sequences from the
progenitor library Gm-c1013 (from 2 to 3 week old whole
plants of Williams); and 1055 sequences from library
Gm-c1028 (from 'superpod' plants whose seedlings were
inoculated with *Bradyrhizobium japonicum*, courtesy of Dr.
Gary Stacey). The 5' ESTs of the source clones from the
different progenitor libraries was used to select
simulations, or a representative of each contig, which were
retacked to form library Gm-1083. The cDNA clones of the
retacked Gm-1083 library were then sequenced at the 3'
end. The contig analysis to select unique genes was
performed by the Laboratory of Ernest Reitzel, Center for
Computational Genomics and Bioinformatics, University of
Minnesota. <http://web.inyte.com/rapid4273324/rapid4273324.html>
Retacking was performed by Inyte Genomes, St. Louis,
<http://www.inyte.com>, and is sequenced by the Keck
Center for Comparative and Functional Genomics, University
of Illinois. <http://www.inyte.com/rapid4273324/rapid4273324.html>
Note: The corresponding 5' EST from each clone in the